

## Amendments to the Claims

1. – 29. (Canceled)

30. (Previously Presented) A method of determining the quinolone resistance of an *Enterobacteriaceae* species selected from the group consisting of *Escherichia coli*, *Citrobacter freundii*, *Enterobacter aerogenes*, *Enterobacter cloacae*, *Klebsiella oxytoca*, *Klebsiella Pneumoniae*, *Providencia stuartii* and *Serratia marcescens* in a sample, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NOS:9-16, or a complementary sequence thereof, respectively, the presence of hybridization with a nucleic acid indicating the quinolone susceptibility of the respective species.

31. (Previously Presented) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:9, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Escherichia coli* in the sample.

32. (Previously Presented) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:10, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Citrobacter freundii* in the sample.

33. (Previously Presented) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:11, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Enterobacter aerogenes* in the sample.

34. (Previously Presented) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:12, or a complementary

sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Enterobacter cloacae* in the sample.

35. (Previously Presented) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:13, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Klebsiella oxytoca* in the sample.

36. (Previously Presented) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:14, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Klebsiella pneumoniae* in the sample.

37. (Previously Presented) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:15, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Providencia stuartii* in the sample.

38. (Previously Presented) The method of determining the quinolone resistance status of an *Enterobacteriaceae* species of Claim 30, comprising combining the sample with a nucleic acid probe, wherein the probe selectively hybridizes to a nucleic acid of SEQ ID NO:16, or a complementary sequence thereof, the presence of hybridization indicating quinolone susceptibility of the *Serratia marcescens* in the sample.

39. (New) The method of claim 30, wherein hybridation of the probe to the nucleic acid sequence of SEQ ID NOs: 1-9 indicates that the *Enterobacteriaceae* species is susceptible to quinolone and a one or more base pair mismatch of the probe to the nucleic acid sequence of one or more of SEQ ID NOs: 1-9 indicates that *Enterobacteriaceae* species is resistant to quinolone.

40. (New) The method of claim 30, wherein the probe is from about 10 to 50 nucleotides in length.

41. (New) The method of claim 30, wherein the probe consists of the nucleic acid sequence set forth as one of SEQ ID NOs: 25-33.